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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/533,466

DATE: 03/29/2001  
TIME: 16:16:47

Input Set : A:\21416942.app  
Output Set: N:\CRF3\03292001\I533466.raw

3 <110> APPLICANT: COLLART, FRANK R.  
4 HUBERMAN, ELIEZER  
5 JOACIMIAK, ANDRZEJ  
6 ZHANG, RONGGUANG  
7 WESTBROOK, EDWIN M.  
9 <120> TITLE OF INVENTION: USE OF CRYSTAL STRUCTURE OF BACTERIAL IMP DEHYDROGENASE  
10 TO DESIGN INHIBITORS OF BACTERIAL GROWTH  
12 <130> FILE REFERENCE: 21416/90042  
14 <140> CURRENT APPLICATION NUMBER: 09/533,466  
15 <141> CURRENT FILING DATE: 2000-03-23  
17 <160> NUMBER OF SEQ ID NOS: 23  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 15  
23 <212> TYPE: PRT  
24 <213> ORGANISM: Streptococcus pyogenes  
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28 1 5 10 15  
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32 <211> LENGTH: 15  
33 <212> TYPE: PRT  
34 <213> ORGANISM: Bacillus subtilis  
36 <400> SEQUENCE: 2  
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38 1 5 10 15  
41 <210> SEQ ID NO: 3  
42 <211> LENGTH: 15  
43 <212> TYPE: PRT  
44 <213> ORGANISM: Escherichia coli  
46 <400> SEQUENCE: 3  
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48 1 5 10 15  
51 <210> SEQ ID NO: 4  
52 <211> LENGTH: 15  
53 <212> TYPE: PRT  
54 <213> ORGANISM: Bacillus subtilis  
56 <400> SEQUENCE: 4  
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58 1 5 10 15  
61 <210> SEQ ID NO: 5  
62 <211> LENGTH: 15  
63 <212> TYPE: PRT  
64 <213> ORGANISM: Mycobacterium tuberculosis  
66 <400> SEQUENCE: 5  
67 Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val  
68 1 5 10 15

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71 <210> SEQ ID NO: 6
72 <211> LENGTH: 15
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
76 <400> SEQUENCE: 6
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78   1             5             10             15
81 <210> SEQ ID NO: 7
82 <211> LENGTH: 15
83 <212> TYPE: PRT
84 <213> ORGANISM: Mus musculus
86 <400> SEQUENCE: 7
87 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys Gly Arg
88   1             5             10             15
91 <210> SEQ ID NO: 8
92 <211> LENGTH: 15
93 <212> TYPE: PRT
94 <213> ORGANISM: Arabidopsis thaliana
96 <400> SEQUENCE: 8
97 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys Gly Arg
98   1             5             10             15
101 <210> SEQ ID NO: 9
102 <211> LENGTH: 15
103 <212> TYPE: PRT
104 <213> ORGANISM: Leishmania donovani
106 <400> SEQUENCE: 9
107 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys Gly Arg
108   1             5             10             15
111 <210> SEQ ID NO: 10
112 <211> LENGTH: 15
113 <212> TYPE: PRT
114 <213> ORGANISM: Saccharomyces cerevisiae
116 <400> SEQUENCE: 10
117 Thr Gly Ser Ile Cys Ile Thr Gln Lys Val Met Ala Cys Gly Arg
118   1             5             10             15
121 <210> SEQ ID NO: 11
122 <211> LENGTH: 15
123 <212> TYPE: PRT
124 <213> ORGANISM: Drosophila melanogaster
126 <400> SEQUENCE: 11
127 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Met Ala Cys Gly Arg
128   1             5             10             15
131 <210> SEQ ID NO: 12
132 <211> LENGTH: 23
133 <212> TYPE: PRT
134 <213> ORGANISM: Streptococcus pyogenes
136 <400> SEQUENCE: 12
137 Met Ala Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala
138   1             5             10             15

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140 Asp Lys Leu Val Pro Glu Gly
141      20
144 <210> SEQ ID NO: 13
145 <211> LENGTH: 23
146 <212> TYPE: PRT
147 <213> ORGANISM: Bacillus subtilis
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150 Met Ser Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala
151   1      5      10      15
153 Asp Lys Leu Val Pro Glu Gly
154      20
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158 <211> LENGTH: 24
159 <212> TYPE: PRT
160 <213> ORGANISM: Escherichia coli
162 <400> SEQUENCE: 14
163 Met Lys Lys Gly Ser Ser Asp Arg Tyr Phe Gln Gly Ser Val Asn Glu
164   1      5      10      15
166 Ala Asn Lys Leu Val Pro Glu Gly
167      20
170 <210> SEQ ID NO: 15
171 <211> LENGTH: 21
172 <212> TYPE: PRT
173 <213> ORGANISM: Bacillus subtilis
175 <400> SEQUENCE: 15
176 Met Glu Lys Gly Ser Lys Asp Arg Tyr Phe Gln Glu Glu Asn Lys Lys
177   1      5      10      15
179 Phe Val Pro Glu Gly
180      20
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184 <211> LENGTH: 30
185 <212> TYPE: PRT
186 <213> ORGANISM: Mycobacterium tuberculosis
188 <400> SEQUENCE: 16
189 Met Arg Gly Arg Gly Gly Ala Thr Ser Tyr Ser Lys Asp Arg Tyr Phe
190   1      5      10      15
192 Ala Asp Asp Ala Leu Ser Glu Asp Lys Leu Val Pro Glu Gly
193   20      25      30
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197 <211> LENGTH: 23
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 17
202 Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
203   1      5      10      15
205 Lys Ile Lys Val Ala Gln Gly
206      20
209 <210> SEQ ID NO: 18
210 <211> LENGTH: 23

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211 <212> TYPE: PRT
212 <213> ORGANISM: Mus musculus
214 <400> SEQUENCE: 18
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218 Lys Ile Lys Val Ala Gln Gly
219           20
222 <210> SEQ ID NO: 19
223 <211> LENGTH: 27
224 <212> TYPE: PRT
225 <213> ORGANISM: Arabidopsis thaliana
227 <400> SEQUENCE: 19
228 Met Glu Arg Gly Asp Ala Lys Gly Ala Ala Met Ser Arg Tyr Tyr His
229   1           5           10           15
231 Asn Glu Met Asp Lys Met Lys Val Ala Gln Gly
232           20           25
235 <210> SEQ ID NO: 20
236 <211> LENGTH: 27
237 <212> TYPE: PRT
238 <213> ORGANISM: Leishmania donovani
240 <400> SEQUENCE: 20
241 Met Gln Lys Thr Gly Thr Lys Gly Asn Ala Ser Thr Ser Arg Tyr Phe
242   1           5           10           15
244 Ser Glu Ser Asp Ser Val Leu Val Ala Gln Gly
245           20           25
248 <210> SEQ ID NO: 21
249 <211> LENGTH: 21
250 <212> TYPE: PRT
251 <213> ORGANISM: Drosophila melanogaster
253 <400> SEQUENCE: 21
254 Met Thr Lys Gly Ser Asp Gln Arg Tyr Leu Gly Asp Gln Thr Lys Leu
255   1           5           10           15
257 Lys Ile Ala Gln Gly
258           20
261 <210> SEQ ID NO: 22
262 <211> LENGTH: 23
263 <212> TYPE: PRT
264 <213> ORGANISM: Saccharomyces cerevisiae
266 <400> SEQUENCE: 22
267 Met Ser Gln Gly Lys Glu Ser Gly Lys Arg Tyr Leu Ser Glu Asn Glu
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270 Ala Val Gln Val Ala Gln Gly
271           20
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275 <211> LENGTH: 477
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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281      polypeptide
283 <220> FEATURE:
284 <221> NAME/KEY: MOD_RES
285 <222> LOCATION: (1)..(477)
286 <223> OTHER INFORMATION: "Xaa" represents selenomethionine
288 <400> SEQUENCE: 23
289 Ser Asn Trp Asp Thr Lys Phe Leu Lys Lys Gly Tyr Thr Phe Asp Asp
290   1          5          10          15
292 Val Leu Leu Ile Pro Ala Glu Ser His Val Leu Pro Asn Glu Val Asp
293          20          25          30
295 Leu Lys Thr Lys Leu Ala Asp Asn Leu Thr Leu Asn Ile Pro Ile Ile
296          35          40          45
W--> 298 Thr Ala Ala Xaa Asp Thr Val Thr Gly Ser Lys Xaa Ala Ile Ala Ile
299          50          55          60
W--> 301 Ala Arg Ala Gly Gly Leu Gly Val Ile His Lys Asn Xaa Ser Ile Thr
302   65          70          75          80
304 Glu Gln Ala Glu Glu Val Arg Lys Val Lys Arg Ser Glu Asn Gly Val
305          85          90          95
307 Ile Ile Asp Pro Phe Phe Leu Thr Pro Glu His Lys Val Ser Glu Ala
308          100         105         110
W--> 310 Glu Glu Leu Xaa Gln Arg Tyr Arg Ile Ser Gly Val Pro Ile Val Glu
311          115         120         125
W--> 313 Thr Leu Ala Asn Arg Lys Leu Val Gly Ile Ile Thr Asn Arg Asp Xaa
314          130         135         140
W--> 316 Arg Phe Ile Ser Asp Tyr Asn Ala Pro Ile Ser Glu His Xaa Thr Ser
317  145         150         155         160
319 Glu His Leu Val Thr Ala Ala Val Gly Thr Asp Leu Glu Thr Ala Glu
320          165         170         175
322 Arg Ile Leu His Glu His Arg Ile Glu Lys Leu Pro Leu Val Asp Asn
323          180         185         190
325 Ser Gly Arg Leu Ser Gly Leu Ile Thr Ile Lys Asp Ile Glu Lys Val
326          195         200         205
328 Ile Glu Phe Pro His Ala Ala Lys Asp Glu Phe Gly Arg Leu Leu Val
329          210         215         220
331 Ala Ala Ala Val Gly Val Thr Ser Asp Thr Phe Glu Arg Ala Glu Ala
332  225         230         235         240
334 Leu Phe Glu Ala Gly Ala Asp Ala Ile Val Ile Asp Thr Ala His Gly
335          245         250         255
337 His Ser Ala Gly Val Leu Arg Lys Ile Ala Glu Ile Arg Ala His Phe
338          260         265         270
340 Pro Asn Arg Thr Leu Ile Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala
341          275         280         285
343 Arg Ala Leu Tyr Asp Ala Gly Val Asp Val Val Lys Val Gly Ile Gly
344          290         295         300
346 Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val Pro
347  305         310         315         320
349 Gln Val Thr Ala Ile Tyr Asp Ala Ala Val Ala Arg Glu Tyr Gly
350          325         330         335
352 Lys Thr Ile Ile Ala Asp Gly Gly Ile Lys Tyr Ser Gly Asp Ile Val

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/533,466

DATE: 03/29/2001

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Input Set : A:\21416942.app

Output Set: N:\CRF3\03292001\I533466.raw

L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23